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Archive

 Bacterial strain

Cupriavidus gilardii (LMG 5886, CCM 4866, DSM 17292)

BacDive ID	Type strain	Strain Designation
2041	✓	4325

Culture col. no.

LMG 5886 CCM 4866 DSM 17292 ATCC 700815 CCUG 38401 4 more

NCBI tax ID(s) Special Collections

82541 DSMZ CCUG JCM CIP

History

DSMZ <- CCUG <- P. Vandamme, LMG, Gent <- D. Monget, Api, France (*Alcaligenes faecalis*) <- G. L. Gilardi, USA

JCM <-- LMG 5886 <-- D. Monget API 141-2-84 <-- G. Gilandi 4325.

CIP <- 1999, CCUG <- P. Vandamme, LMG, Gent, Belgium, *Alcaligenes faecalis* subsp. *faecalis* <- D. Monget, API, France: strain API141-2-84, *Alcaligenes faecalis* <- G.L. Gilardi, USA: strain 4325

Links

 StrainInfo 

 Show all  Names & IDs  Morphology  Cultivation

 Physiology & metabolism  Isolation & Environment  Interaction & safety

 Sequences  Predictions  Literature  References

Cupriavidus gilardii 4325 is an obligate aerobe, Gram-negative, motile bacterium that was isolated from whirlpool.

Gram-negative motile rod-shaped obligate aerobe
16S sequence Bacteria

Name and taxonomic classification

 StrainInfo SI-ID 765

LMG 5886,ATCC 700815,CCUG 38401,JCM 11283,CIP 105966,CCM 4866,DSM 17292,BCRC 17471,CCRC 17471,CFBP 6736

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@ref 20215	
Last LPSN update 2026-05-29 08:25:24	
Domain <i>Bacteria</i>	
Phylum <i>Pseudomonadota</i>	
Class <i>Betaproteobacteria</i>	
Order <i>Burkholderiales</i>	
Family <i>Burkholderiaceae</i>	
Genus <i>Cupriavidus</i>	
Species <i>Cupriavidus gilardii</i>	
Full scientific name <i>Cupriavidus gilardii</i> (Coenye et al. 1999) Vandamme and Coenye 2004	
Synonyms (2) <i>Ralstonia gilardii</i> <i>Wautersia gilardii</i>	

BacDive ID	Other strains from <i>Cupriavidus gilardii</i> (9)	Type strain
138273	<i>C. gilardii</i> CIP 105941, CCUG 24719, LMG 15537	×
138274	<i>C. gilardii</i> GLG 4962, CIP 105942, CCUG 15433, LMG 15541, ...	×
144108	<i>C. gilardii</i> CCUG 23091	×
144355	<i>C. gilardii</i> CCUG 24724, LMG 15540	×
149786	<i>C. gilardii</i> CCUG 38402, LMG 5887	×
149787	<i>C. gilardii</i> CCUG 38403, LMG 5888	
149790	<i>C. gilardii</i> CCUG 38406, LMG 5910	
149791	<i>C. gilardii</i> CCUG 38407, LMG 5913	
175146	<i>C. gilardii</i> Dres_CurprGil_02, DSM	

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Morphology

Cell morphology

@ref	Gram stain	Cell shape	Motility	Confidence	
119616	negative	rod-shaped	✓		
125439	negative			94.922	 
125438	negative			98.5	 

Culture and growth conditions

Culture medium

@ref	Name	Growth	Medium link	Composition	
6877	CASO AGAR (MERCK 105458) (DSMZ Medium 220)	✓	Medium recipe at MediaDive 	Name: CASO AGAR (Merck 105458) (DSMZ Medium 220) Composition: Agar 15.0 g/l Casein peptone 15.0 g/l NaCl 5.0 g/l Soy peptone 5.0 g/l Distilled water	
40276	MEDIUM 3 - Columbia agar	✓		Columbia agar (39.000 g);distilled water (1000.000 ml)	
119616	CIP Medium 72	✓	Medium recipe at CIP		
119616	CIP Medium 3	✓	Medium recipe at CIP		
6877	TRYPTICASE SOY BROTH AGAR (DSMZ Medium 535)	✓	Medium recipe at MediaDive 	Name: TRYPTICASE SOY BROTH AGAR (DSMZ Medium 535) Composition: Trypticase soy broth 30.0 g/l Agar 15.0 g/l Distilled water	
	NUTRIENT		Medium recipe		

Culture temp

×

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@ref	Growth	Type	Temperature (°C)	
6877	positive	growth	37	
40276	positive	growth	30	
67770	positive	growth	30	
119616	positive	growth	25-41	
119616	negative	growth	5	
119616	negative	growth	10	

Physiology and metabolism

Oxygen tolerance

@ref	Oxygen tolerance	Confidence	
119616	obligate aerobe		
125438	aerobe	90.532	
125439	obligate aerobe	99.883	

Spore formation

@ref	Spore formation	Confidence	
125439	✗	98.574	

Halophily

@ref	Salt	Growth	Tested relation	Concentration	
119616	NaCl	positive	growth	0-4 %	
119616	NaCl	✗	growth	6 %	
119616	NaCl	✗	growth	8 %	
119616	NaCl	✗	growth	10 %	

Metabolite utilization

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@ref	Chebi-ID	Metabolite	Utilization activity	Kind of utilization tests
68369	17128  ChEBI	adipate	+	assimilation
68371	18305  ChEBI	arbutin	+	builds acid from
68369	29016  ChEBI	arginine	-	hydrolysis
119616	16947  ChEBI	citrate	-	carbon source
68371	17108  ChEBI	D-arabinose	-	builds acid from
68371	18333  ChEBI	D-arabitol	-	builds acid from
68371	15824  ChEBI	D-fructose	+	builds acid from
68371	28847  ChEBI	D-fucose	-	builds acid from
68371	12936  ChEBI	D-galactose	-	builds acid from
68371	17634  ChEBI	D-glucose	+	builds acid from
	17634 			

Antibiotic resistance

@ref	Metabolite	Is sensitive	Is resistant	
119616	0129 (2,4-Diamino-6,7-di-iso-propylpteridine phosphate)	✗	✓	

Metabolite production

@ref	Chebi-ID	Metabolite	Produced
68369	35581  ChEBI	indole	✗
119616	35581  ChEBI	indole	✗

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Metabolite tests

@ref

Chebi-ID

Metabolite

Indole test

68369

35581

ChEBI

indole

-

from API 20NE

Enzymes

@ref	Value	Activity	Ec	
68382	acid phosphatase	+	3.1.3.2 BRENDA	from API zym
119616	alcohol dehydrogenase	-	1.1.1.1 BRENDA	
68382	alkaline phosphatase	+	3.1.3.1 BRENDA	from API zym
68382	alpha-chymotrypsin	-	3.4.21.1 BRENDA	from API zym
68382	alpha-fucosidase	-	3.2.1.51 BRENDA	from API zym
68382	alpha-galactosidase	-	3.2.1.22 BRENDA	from API zym
68382	alpha-glucosidase	-	3.2.1.20 BRENDA	from API zym
68382	alpha-mannosidase	-	3.2.1.24 BRENDA	from API zym
119616	amylase	-		
68369	arginine dihydrolase	-	3.5.3.6 BRENDA	from API 20NE
119616	beta-galactosidase	-	3.2.1.23 BRENDA	
68382	beta-galactosidase	-	3.2.1.23 BRENDA	from API zym

API zym

@ref	Control	Alkaline phosphatase	Esterase (C 4)	Esterase Lipase (C 8)	Lipase (C 14)
119616	-	+	+	+	-

API 20NE

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@ref	NO3	TRP	GLU_ Ferm	ADH (Arg)	URE	ESC	GEL	PNPG	GLU_ Assim	ARA	MNE	MAN	NAG	MAL	GNT	CAP
6877	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
6877	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+

API 50CHac ⓘ

@ref	Q	GLY	ERY	DARA	LARA	RIB	DXYL	LXYL	ADO	MDX	GAL	GLU	FRU	MNE	SBE	RHA
119616	n.d.	-	-	-	-	+	-	-	-	-	-	+	+	+	-	-

API biotype100 ⓘ

@ref	Q	GLU	FRU	GAL	TRE	MNE	SBE	MEL	SAC	RAF	MTE	MAL	LAC	LTE	MbGa	MaGa
119616	n.d.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Isolation, sampling and environmental information

Isolation source categories ⓘ

#Engineered #Built environment #Water reservoir (Aquarium/pool) 

Isolation

@ref	Sample type	Country	Country ISO 3 Code	Continent	
6877	whirlpool	USA	USA	North America	
54234	Whirl pool				
67770	Whirl pool				
119616	Environment, Whirl pool				

Taxonmaps

69479

Global distribution of 16S sequence [EU024163](#) (>99% seq

Microbeatlas     BETA

Interaction and safety

Risk assessment

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 Aquatic Samples	204
 Soil Samples	301
 Animal Samples	739
 Plant Samples	466
Total Samples	1710

@ref	Pathogenicity human	Biosafety level	Biosafety level comment	
6877	yes, in single cases	1	Risk group (German classification) According to TRBA 466	
119616		1	Risk group (French classification) According to TRBA 466	

Sequence information

Genome sequences

@ref	Description	Assembly level	INSDC accession	BV-BRC accession
67770	ASM1300461v1 assembly for Cupriavidus gilardii ATCC 700815	contig	GCA_013004615 	82541.17 
67770	ASM880191v1 assembly for Cupriavidus gilardii CCUG 38401	contig	GCA_018801911 	
124043	ASM3952278v1 assembly for Cupriavidus gilardii JCM 11283	scaffold	GCA_039522785 	

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Genome browser: GCA_013004615

Contigs

JABEMD010000001

JABEMD010000010

JABEMD010000100

Bakta annotation

CDSs: 5042 tRNAs: 52 rRNAs: 2
ncRNAs: 9 regulatory elements: 14
pseudogenes: 14

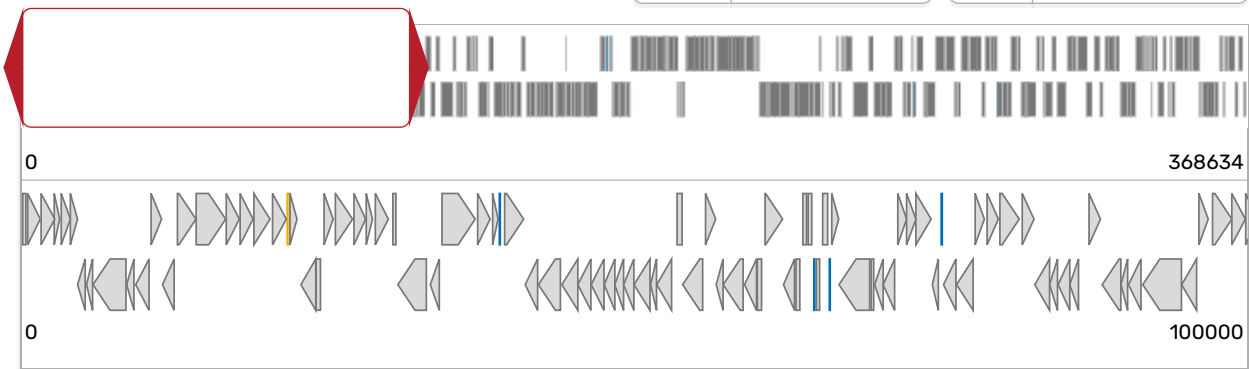
JABEMD010000001.1, whole genome
shotgun sequence

Start

0

End

100000



Legend: ☐ CDS ☐ tRNA ☐ rRNA ☐ ncRNA ☐ regulatory ☐ pseudogene

Show feature table

16S sequences

@ref	Description	Accession	Length	Database	NCBI tax ID
20218	Cupriavidus gilardii strain CIP 105966 16S ribosomal RNA gene, partial sequence	EU024163	1315	ENA	82541
6877	Ralstonia gilardii 16S ribosomal RNA gene, complete sequence	AF076645	1451	silva	NCBI

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GC content

@ref	GC-content (mol%)	Method	
6877	68-69		
67770	68.3	thermal denaturation, midpoint method (Tm)	

Genome-based predictions

Predictions

Predictions from [Deep Learning for Genome Sequence Data. R package version 0.3.1](#) based on:
ASM1300461v1 assembly for Cupriavidus gilardii ATCC 700815
BV-BRC: 82541.17

@ref	Trait	Model	Prediction	Confidence in %	In train
125439	oxygen_tolerance	BacteriaNet ⓘ	obligate aerobe	99.88	no
125439	gram_stain	BacteriaNet ⓘ	negative	94.92	no
125439	motility	BacteriaNet ⓘ	yes	61.81	no
125439	spore_formation	BacteriaNet ⓘ	no	98.57	no

Predictions from [bacterial phenotypic traits through improved machine learning using high-quality, curated datasets](#) based on:
Cupriavidus gilardii strain ATCC 700815
PATRIC: 82541.17

@ref	Trait	Model	Prediction	Confidence in %	In training d
125438	gram-positive	gram-positive ⓘ	no	98.50	no
125438	anaerobic	anaerobic ⓘ	no	98.56	no
125438	aerobic	aerobic ⓘ	yes	90.53	no
125438	spore-forming	spore-forming ⓘ	no		
125438	thermophilic	thermophile ⓘ	no		
125438	flagellated	motile2+ ⓘ	yes		

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Literature

Literature BIB_{TEX}

Topic	Title	Authors	Journal	DOI
Phylogeny	First case report of infection due to Cupriavidus gilardii in a patient without immunodeficiency: a case report.	Kobayashi T, Nakamura I, Fujita H, Tsukimori A, Sato A, Fukushima S, Ohkusu K, Matsumoto T.	BMC Infect Dis	10.1186/s
	Characterization of newly isolated thermotolerant bacterium Cupriavidus sp. CB15 from composting and its ability to produce polyhydroxyalkanoate from glycerol.	Yootoum A, Jantanasakulwong K, Rachtanapun P, Moukamnerd C, Chaiyaso T, Pumas C, Tanadchangsang N, Watanabe M, Fukui T, Insomphun C.	Microb Cell Fact	10.1186/s12934-0
Genetics	Comparative Genomics Reveals a Well-Conserved Intrinsic Resistome in the Emerging Multidrug-Resistant Pathogen	Ruiz C, McCarley A, Espejo ML, Cooper KK, Harmon DE.	mSphere	10.1128/n

References

#6877	Leibniz Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH ; Curators of the DSMZ; DSM 17292
#20215	Parte, A.C., Sardà Carbasse, J., Meier-Kolthoff, J.P., Reimer, L.C. and Göker, M.: List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ . IJSEM (DOI 10.1099/ijsem.0.004772)
#20218	Verslyppe, B., De Smet, W., De Baets, B. introduces electronic passports for microorganisms . J. Symp. Microbiol. 37: 42 - 50 2014 (DOI 10.1016/j.syapm.2014.05.001)
#40276	; Curators of the CIP;
#54234	Culture Collection University of Goethe CCUG 38401
#67770	Japan Collection of Microorganism (JCM) ; Curators of the JCM;
#68369	Automatically annotated from API 20NE .

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#68371	Automatically annotated from API 50CH acid .
#68382	Automatically annotated from API zym .
#69479	João F Matias Rodrigues, Janko Tackmann,Gregor Rot, Thomas SB Schmidt, Lukas Malfertheiner, Mihai Danaila,Marija Dmitrijeva, Daniela Gaio, Nicolas Näpflin and Christian von Mering. University of Zurich.: MicrobeAtlas 1.0 beta .
#119616	Collection of Institut Pasteur ; Curators of the CIP; CIP 105966
#124043	Isabel Schober, Julia Koblitz: Data extracted from sequence databases, automatically matched based on designation and taxonomy .
#125438	Julia Koblitz, Lorenz Christian Reimer, Rüdiger Pukall, Jörg Overmann: Predicting bacterial phenotypic traits through improved machine learning using high-quality, curated datasets . 2024 (DOI 10.1101/2024.08.12.607695)
#125439	Philipp Münch, René Mreches, Martin Binder, Hüseyin Anil Gündüz, Xiao-Yin To, Alice McHardy: deepG: Deep Learning for Genome Sequence Data. R package version 0.3.1 .
#126262	A. Lissin, I. Schober, J. F. Witte, H. Lüken, A. Podstawka, J. Koblitz, B. Bunk, P. Dawyndt, P. Vandamme, P. de Vos, J. Overmann, L. C. Reimer: StrainInfo—the central database for linked microbial strain identifiers . (DOI 10.1093/database/baaf059)

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